SEQUENCE LISTING

<110> Cahoon, Rebecca E.
      Lee, Jian-Ming
      Tao, Youn

<120> PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE

<130> BB1297

<140> US/09/857,557
<141> 2001-09-22

<150> 60/110,865
<151> 1998-12-04

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tggctgcact caaggcatcg ttccgggggtg agctcagcgc cgcttccttc ctcgactcca 240
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tggttcaact ggttccatag gaacacagan attggacatt gttgcggaga tcctgataa 480
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Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn
            20   25   30

Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
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Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg
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ggttgtgcag ggctgaagcc tacagttgct gcaattgaag ctggtaaaga catagcattg 180
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aatatgggaa ggaagatcac agtagattct gctactttat tcaacaaggg tttagaagtt 480
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2

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cagtctatca tacactctat ggttgaaacc caggattcat ctgtcctagc tcagttggga 600
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cgctgctaat gagaaggccg tggagttgtt cattgacgag aagattagct acctggacat 720
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              20                  25                  30

Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
          35                  40                  45

Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
      50                  55                  60

Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
65                  70                  75                  80

Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
              85                  90                  95

Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
             100                 105                 110

Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro Xaa Asp Arg Leu Lys Asp
         115                 120                 125

Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
         130                 135                 140

Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
145                 150                 155                 160

Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
             165                 170                 175
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3

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Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
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Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
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Leu Tyr Thr Leu Ser Trp Pro Asp Arg
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cggcacgagg tttaaaccag acgtcgagtc gagcattaac tcagtcaggg tggccatggc   180
gctcaaggtc gtctctttcc ccggggactt ggccgcggtc tcattcctcg actccaacag   240
aggaggagct ttcaaccagc tcaaagtgga cctcccgttt caaacgaggg acagaagagc   300
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tcgagccgtt gttgaacctg ggaggaggtc atgggatggc cccaagccta tctcaattgt   420
tggctcaacc ggttctattg cacacagac attggacata gttgcggaga atccagataa   480
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aacattcaaa ccaaagcttg ttgctgtaag aaatgagtca ttagttgatg agctaaagga   600
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ggttgctcgc cacccagatg cagttacagt tgttactggg atagtagggt gtgcaggact   720
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tcctgctgat tctgagcact ctgctatatt tcagtgtata caaggcttgc ccgaaggagc   900
acttcgccgc attattttga ctgcatcagg tggtgctttc agggactggc cagttgacaa   960
gttgaaagaa gtaaaagttg ctgatgcttt aaagcacccg aactggaata tggggaagaa  1020
gattactgta gattctgcta cattattcaa caagggttta gaagttattg aagcacatta  1080
tttatttggt gctgaatacg atgacattga aattgtgatc cacccacaat ctatcataca  1140
ctctatgatt gaaacccagg attcatctgt gttggctcaa ctgggatggc cagatatgcg  1200
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agtagcattg tacactactg ccgtgccagc tccatgcata gtcagcagct ggccactctc  1680
tagctatatc tagatgcgag agaattttaa ggatgtaaat catgccttca catgaataaa  1740
tcgttcgtcc gtgcgttgtg tattcatgta aattttgacg gatggtcaag taaaaataac  1800
aatggcaaat taatttaggg aaaaaaaaa aaaaaaaact cgaggggggg cccggtaccc  1860
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Phe Leu Asp Ser Asn Arg Gly Gly Ala Phe Asn Gln Leu Lys Val Asp
            20                  25                  30
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4

Leu Pro Phe Gln Thr Arg Asp Arg Arg Ala Val Ser Leu Arg Arg Thr
        35   40   45

Cys Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala
        50   55   60

Val Val Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser
65   70   75   80

Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val
                85   90   95

Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser
                100   105   110

Asn Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu
        115   120   125

Val Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu
        130   135   140

Ala Asp Cys Asp Trp Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val
145   150   155   160

Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile
                165   170   175

Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly
                180   185   190

Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro
        195   200   205

Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala
        210   215   220

Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu
225   230   235   240

Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg
                245   250   255

Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu
                260   265   270

Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala
        275   280   285

Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe
        290   295   300

Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile
305   310   315   320

Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu
                325   330   335

Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro
                340   345   350

5

Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys
        355   360   365

·Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro
        370   375   380

Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr
385   390   395   400

Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp
            405   410   415

Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys
            420   425   430

Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile
        435   440   445

Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro
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Ser Thr Gly Leu Ser Pro Val Pro Val
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gatgaactca agaggctttt ggctgatgtg atcacaaac ccgaaatcat ccctggagag 480
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caatccatca tacattcctt ggttgaaacg cangattcat ctgttaatgc acagttgggg 1020
atacctgaca tgcgcttacc gctcctttat acattatctt ggccagaaag aatctattgc 1080
tctgaagtaa cttggcctcg tcttgatctt agcaagtatg gttctctaac attttatgca 1140

6

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ccggatgaca agaagtttcc atcggtgaat ctttgctatg ctgcgggacg tgctggaggc 1200
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Ser Ser Asn Asn Ser Thr Lys Leu Pro Gly Ser Phe Ser Leu Lys Arg
               20                  25                  30

Lys Asp Ser Asp Thr Thr Val Glu Arg Arg Val Tyr Cys Ser Ala Ala
               35                  40                  45

Ala Gln Ser Pro Pro Pro Ala Trp Pro Gly Thr Ala Ile Pro Glu Pro
         50                  55                  60

Ser Asp Phe Lys Thr Trp Asp Gly Gln Lys Pro Ile Ser Val Leu Gly
 65                  70                  75                  80

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Ser Ile Val Ala Glu Phe
               85                  90                  95

Pro Glu Arg Phe Lys Val Val Ser Leu Ala Ala Gly Ser Asn Ile Thr
              100                 105                 110

Leu Leu Ala Asp Gln Ile Lys Thr Phe Lys Pro Glu Val Val Gly Leu
             115                 120                 125

Arg Asn Glu Ser Leu Ile Asp Glu Leu Lys Glu Ala Leu Ala Asp Val
             130                 135                 140

Asp His Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Ala
145                 150                 155                 160

Ala Arg His Pro Asp Ala Thr Thr Val Val Thr Gly Ile Val Gly Cys
                 165                 170                 175

Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
             180                 185                 190
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7

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Ala Leu Ala Asn Lys Glu Thr Met Ile Ala Gly Ala Pro Phe Val Leu
        195             200             205

Pro Leu Ala His Lys His Asn Ile Lys Ile Leu Pro Ala Asp Ser Glu
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His Ser Ala Ile Phe Gln Ser Ile Gln Gly Leu Pro Lys Gly Ala Leu
225             230             235             240

Arg Lys Ile Leu Leu Thr Gly Ser Gly Gly Ala Phe Arg Glu Trp Pro
            245             250             255

Ala Glu Lys Met Lys Asp Ile Lys Leu Ala Asp Ala Leu Lys His Pro
            260             265             270

Ile Trp Ser Leu Gly Arg Lys Ile Thr Ile Asp Ser Ala Thr Leu Phe
        275             280             285

Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Ser
        290             295             300

Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
305             310             315             320

Leu Val Glu Thr Xaa Asp Ser Ser Val Asn Ala Gln Leu Gly Ile Pro
            325             330             335

Asp Met Arg Leu Pro Leu Leu Tyr Thr Leu Ser Trp Pro Glu Arg Ile
            340             345             350

Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Ser Lys Tyr Gly
        355             360             365

Ser Leu Thr Phe Tyr Ala Pro Asp Asp Lys Lys Phe Pro Ser Val Asn
        370             375             380

Leu Cys Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu
385             390             395             400

Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Val Glu Glu Lys Ile
            405             410             415

Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Gln Glu His
            420             425             430

Gln Lys Glu Leu Val Ala Ser Pro Ser Leu Glu Glu Ile Ile His Tyr
            435             440             445

Asp Gln Trp Ala Arg Gln Tyr Ala Ala Ser Leu Gln Lys Xaa Phe Lys
        450             455             460

Cys Leu Asn Pro Ile Phe Leu Thr Tyr Phe Arg Ser Trp Gly Cys Gly
465             470             475             480

Gly Leu Leu Ala Thr Ala Ser Ile Phe Cys Lys Cys Ile Val Gly Ser
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Ser Ile Leu
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8

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actggttcaa ttggaactca gacactagat attgtggcag agaatccaga taagtttaaa 180
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aagcctcaac ttgttgctgt tagaaatgag tccctaattg ctgaacttga agaggccttg 300
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cgtcacccag atgcagttag tgtagtcaca ggaatagtag gctgtgcagg actgaagcca 420
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ttaaagttgc tgatncatta aaacatccta ctggaatatg ggggaaagaa ctgtggactc 720
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Pro Gly Xaa Ala Val Pro Glu Gln Gly Arg Lys Thr Trp Asp Gly Pro
            20   25   30

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
         35   40   45

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu
     50   55   60

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe
 65   70   75   80

Lys Pro Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu
             85   90   95

10

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Glu Glu Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly
            100                 105             110

Glu Gln Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val
            115                 120             125

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
            130                 135             140

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
145                 150                 155                 160

Ala Gly Gly Pro Leu Ser Pro Leu Ala Gln Lys His Asn Val Lys Ile
            165                 170             175

Leu Pro Ala Asp Ser Asp Xaa Ser Ala Ile Phe Gln Cys Ile Gln Gly
            180                 185             190

Leu Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly
            195                 200             205

Ala Phe Arg Gly Trp Pro Val
    210                 215
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<222> (601)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (606)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (625)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (628)
<223> n = A, C, G, or T

<400> 11
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tgcctacctg aggacatgct gctccatgca gcagggccca ccgcccgcct ggccaggccg 180
agccgtcgtg gaacctgaga ggaggtcgtg ggagggcccc aagcccatct ccatcgtcgg 240
ctcaaccggt tccataggaa cacagacatt ggacatcgtt gcggagaacc tgacaagttc 300
ccgggttgtc gcccttgctg ctgggtccaa cgtcactcct ctagctgata aggtgaaaac 360
gttcaaacca aactgggtgg tgttaagaaa cgatccatta cttaacgagc taaaggaagc 420
attaactggt tgtgaaagag atccggatta tccctgggga caagtgcata gaggcgcacc 480
cacccggacc attacatcct acggnatat aggttncaag atcaacctac attncaacat 540
ttaactggaa aatntgcttt gggaacaaaa accttnccag gtgnccttct ctccctncca 600
naacanattg aaatactctg cgatnaanat ctgatatcat ga   642

<210> 12
<211> 94
<212> PRT
<213> Triticum aestivum

<400> 12
Met Gln Gln Gly Pro Pro Pro Ala Trp Pro Gly Arg Ala Val Val Glu
1   5   10   15

Pro Glu Arg Arg Ser Trp Glu Gly Pro Lys Pro Ile Ser Ile Val Gly
            20   25   30

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
        35   40   45

Leu Thr Ser Ser Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
    50   55   60

Pro Leu Ala Asp Lys Val Lys Thr Phe Lys Pro Asn Trp Val Val Leu
65   70   75   80

Arg Asn Asp Pro Leu Leu Asn Glu Leu Lys Glu Ala Leu Thr

12

<210> 13
<211> 360
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (295)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (299)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (313)
<223> n = A, C, G, or T

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<221> unsure
<222> (338)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (352)
<223> n = A, C, G, or T

<400> 13
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tgggctcgct gacattcaaa gctcccgaca acgtgaaata cccatcggta gatctccgcc 180
gtacgcggca gggcgagccg ggggcaccat gacgggattt ttgagtgctg ctaatgagaa 240
ggcgtggagc ttgttcatcg acgaaaagat taactacctt ggacatcttc aaggngggng 300
agaatacctt ttnacgccaa ccgcaacaac tgggtganag ctcctcccca anggggggg 360

<210> 14
<211> 93
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (59)
<223> Xaa = ANY AMINO ACID

<400> 14
Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu
 1   5   10   15

Tyr Thr Leu Ser Trp Pro Asp Arg Val Tyr Cys Ser Glu Val Thr Trp
            20   25   30

Pro Arg Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro
        35   40   45

```
Asp Asn Val Lys Tyr Pro Ser Val Asp Leu Xaa Xaa Tyr Ala Ala Gly
      50                55                60

Arg Ala Gly Gly Thr Met Thr Gly Phe Leu Ser Ala Ala Asn Glu Lys
  65                70                75                80

Ala Trp Ser Leu Phe Ile Asp Glu Lys Ile Asn Tyr Leu
              85                90
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<210> 15
<211> 1847
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (5)..(9)
<223> n = A, C, G, or T

<400> 15
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ccctccctct cccccctcctc gcccagcggc aattaccaca gcctccccag caagccggga   180
tggctgcact caaggcatcg ttccggggtg agctcagcgc cgcttccttc ctcgactcca   240
gcaggggacc tctcgtccag cacaaagtgg attttacgtt tcaaaggaag ggcaaacgag   300
ctatttcact gagaaggaca tgctgttcta tgcaacaggc tccaccacca gcatggcctg   360
ggcgagctgt tgctgagcct ggccggaggt catgggatgg cccaaagcct atctcgattg   420
ttggttcaac tggttccata ggaacacaga cattggacat tgttgcggag aatcctgata   480
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aaacattcaa acctaagttg gttgctgtaa gaaacgaatc attagttgat gaattgaaag   600
aagccttggc tgattgcgaa gagaagccag aaattattcc tggggagcaa ggtgtcatag   660
aagttgctcg ccatccagat gcagttacag ttgtcacagg gatagtaggt tgtgcagggc   720
tgaagcctac agttgctgca attgaagctg gtaaagacat agcattggca aacaaagaga   780
cacttattgc aggtggtcct tttgtgcttc cccttgcaca caaacacaaa gtgaaaattc   840
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cacttcgtcg cattattcta actgcatcag gtggtgcttt cagggactgg ccagttgaca   960
ggctgaaaga tgtaaaagtt gctgacgctt aaagcatcc aaactggaat atgggaagga  1020
agatcacagt agattctgct actttattca acaagggttt agaagttatt gaagcacatt  1080
atttatttgg tgctgaatat gatgacattg agattgtgat tcacccacag tctatcatac  1140
actctatggt tgaaacccag gattcatctg tcctagctca gttgggatgg ccagatatgc  1200
ggttaccaat cttatacacc ttatcatggc cagatagaat ctattgctct gaggtcacct  1260
ggccccgtct ggatctttgc aagttgggtt cactgacatt cagagctcca gacaacgtaa  1320
aatacccatc aatggaccta gcctatgcag ctggccgcgc tggggggcacc atgacaggag  1380
tcctgagcgc tgctaatgag aaggccgtgg agttgttcat tgacgagaag attagctacc  1440
tggacatatt caaggtggtg gagcttacat gtaacgcgca tcggaacgag ctggtaacaa  1500
gcccgtcact ggaggagatc gtccattacg atctgtgggc gaggagatat gcagccagtc  1560
tacaaccatc ttctggcctg agccctgtcc ctgcataata ggtcgtcacg acaacgttgt  1620
acagcaggag ttctaagata tgatgtgttt gtggctcctg tttccatgtt caattttcag  1680
gcctccacat gaataaaatg catctattcc atgtgatttc ttttatggat gaagtgtgcg  1740
aagtcgggtg ggaatcagat gcatcccttt cggtggagtt cttacgtagg gttgagcagc  1800
atttttttaaa aaggtttttt tacctctgca aaaaaaaaaa aaaaaaa         1847
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<210> 16
<211> 472
<212> PRT
<213> Zea mays

<400> 16
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Met Ala Ala Leu Lys Ala Ser Phe Arg Gly Glu Leu Ser Ala Ala Ser
  1               5                10                15
```

14

Phe Leu Asp Ser Ser Arg Gly Pro Leu Val Gln His Lys Val Asp Phe
            20   25   30

Thr Phe Gln Arg Lys Gly Lys Arg Ala Ile Ser Leu Arg Arg Thr Cys
            35   40   45

Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala Val
    50   55   60

Ala Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile
65   70   75   80

Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala
                85   90   95

Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn
            100   105   110

Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu Val
            115   120   125

Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu Ala
            130   135   140

Asp Cys Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile
145   150   155   160

Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile Val
                165   170   175

Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys
            180   185   190

Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe
            195   200   205

Val Leu Pro Leu Ala His Lys His Lys Val Lys Ile Leu Pro Ala Asp
    210   215   220

Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly
225   230   235   240

Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp
            245   250   255

Trp Pro Val Asp Arg Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys
            260   265   270

His Pro Asn Trp Asn Met Gly Arg Lys Ile Thr Val Asp Ser Ala Thr
    275   280   285

Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly
    290   295   300

Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile
305   310   315   320

His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly
                325   330   335

15

Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp
            340   345   350

Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys
            355   360   365

Leu Gly Ser Leu Thr Phe Arg Ala Pro Asp Asn Val Lys Tyr Pro Ser
            370   375   380

Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly
385   390   395   400

Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu
            405   410   415

Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asn
            420   425   430

Ala His Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Glu Ile Val
            435   440   445

His Tyr Asp Leu Trp Ala Arg Arg Tyr Ala Ala Ser Leu Gln Pro Ser
    450   455   460

Ser Gly Leu Ser Pro Val Pro Ala
465   470

<210> 17
<211> 2019
<212> DNA
<213> Glycine max

<400> 17
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tttcgctgat tccttcaagt ctaactgcct cacagcaaaa ttctcaggtg ggtttgcttt 180
taagagaaaa gagcgtagag cagcatctgg aggacgggtt tattgctcag tgcaggcaac 240
accaccacca ccagcctggc cgggacgagc ggttccggaa caaggtcgca agacttggga 300
tggaccaaaa cccatttcaa ttgtggggag tactggttca attggaactc agacactaga 360
tattgtggca gagaatccag ataagtttaa agttgtggca cttgcagctg gttcaaatgt 420
tactcttctt gcagaccagg taaaaagatt taagcctcaa cttgttgctg ttagaaatga 480
gtccctaatt gctgaacttg aagaggcctt gcatgatgtt gaagaaaaac ctgagatcat 540
ccctggagag cagggaatca ttgaggttgc tcgtcaccca gatgcagtta gtgtagtcac 600
aggaatagta ggctgtgcag gactgaagcc aacagttgca gcgatagaag cagggaaaga 660
catagctttg gccaacaaag agacattgat tgctggaggt cctttttgttc ttcctcttgc 720
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tatccagggg ttgccagagg gtgcacttag gagagttatt ttaactgcat ctggaggtgc 840
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tctagaagta attgaagcac attacttgtt tggagctgac tacgatcata ttgagattgt 1020
cattcatcca caatcaatca tacattcaat gattgaaaca caggattcat ctgttcttgc 1080
acaattgggg tggcctgata tgcgtttgcc aatcctctat acattatcat ggcctgacag 1140
gatttattgt tctgaagtca cttggccacg ccttgatctt tgcaagcttg gttcacttac 1200
atttaaaact ccagataatg taaagtatcc atccatgaat cttgcatttt ctgctggccg 1260
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tattgatgaa aagataagct attggaattt attcaaagtt gtggagctaa catgtgagaa 1380
gcatcaaaat gaattggtat cctctccttc ccttgaggaa attattcact atgacctgtg 1440
ggcgcgaaaa tatgctgcta gtctgcaaga ctcttccagc ttcactccta ttcttgcatg 1500
aggatgatta aactagggat gtggctgatg cttcccaatt gcctgctttc accataattt 1560

16

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cttcgggcat tgaacaatgt agaatggtgc attccacaga tgttgaaaat taaataggtt 1620
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atttcatgga aaacgatgtc tttttaatag tcaataggag cctaggaggt tggttggttg 1740
cctatgaatg tgtcaaagtc aagaagggga atggattttc tcatattcaa aatttacatg 1800
atgtggtcaa ctagaagttt tgtatttctc tttttctaat agaattaaat aggtggagtc 1860
ttacaaaaat taacagagat agacacaaaa gttgaccaat caccaatcac tttcataaaa 1920
ggattccttt tcttttcct cagcacacat tcgttggctg atattattat atgaaattgg 1980
tattatttgg atatcatagc taaaaaaaaa aaaaaaaa                         2019
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<210> 18
<211> 475
<212> PRT
<213> Glycine max

<400> 18

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Met Met Ala Leu Asn Ile Ser Ser Pro Ala Glu Val Lys Ser Ile Phe
  1               5                  10                  15

Phe Ala Asp Ser Phe Lys Ser Asn Cys Leu Thr Ala Lys Phe Ser Gly
             20                  25                  30

Gly Phe Ala Phe Lys Arg Lys Glu Arg Arg Ala Ala Ser Gly Gly Arg
         35                  40                  45

Val Tyr Cys Ser Val Gln Ala Thr Pro Pro Pro Ala Trp Pro Gly
     50                  55                  60

Arg Ala Val Pro Glu Gln Gly Arg Lys Thr Trp Asp Gly Pro Lys Pro
 65                  70                  75                  80

Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp
                 85                  90                  95

Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu Ala Ala
             100                 105                 110

Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe Lys Pro
         115                 120                 125

Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu Glu Glu
     130                 135                 140

Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln
145                 150                 155                 160

Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val Val Thr
                 165                 170                 175

Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu
             180                 185                 190

Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly
         195                 200                 205

Gly Pro Phe Val Leu Pro Leu Ala Gln Lys His Asn Val Lys Ile Leu
     210                 215                 220

Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu
225                 230                 235                 240
```

17

Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala
            245   250   255

Phe Arg Asp Trp Pro Val Asp Lys Leu Lys Asp Val Lys Val Ala Asp
            260   265   270   .

Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp
            275   280   285

Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr
            290   295   300

Leu Phe Gly Ala Asp Tyr Asp His Ile Glu Ile Val Ile His Pro Gln
305   310   315   320

Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala
            325   330   335

Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser
            340   345   350

Trp Pro Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp
            355   360   365

Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Thr Pro Asp Asn Val Lys
            370   375   380

Tyr Pro Ser Met Asn Leu Ala Phe Ser Ala Gly Arg Ala Gly Gly Thr
385   390   395   400

Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe
            405   410   415

Ile Asp Glu Lys Ile Ser Tyr Trp Asn Leu Phe Lys Val Val Glu Leu
            420   425   430

Thr Cys Glu Lys His Gln Asn Glu Leu Val Ser Ser Pro Ser Leu Glu
            435   440   445

Glu Ile Ile His Tyr Asp Leu Trp Ala Arg Lys Tyr Ala Ala Ser Leu
    450   455   460

Gln Asp Ser Ser Ser Phe Thr Pro Ile Leu Ala
465   470   475

<210> 19
<211> 1640
<212> DNA
<213> Triticum aestivum

<400> 19
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aaagagcagc ctacctgagg acatgctgct cgatgcagca gggcccaccg cccgcctggc 180
ctggccgagc cgtcgcggaa cccgagagga ggtcgtggga gggccccaag cccatctcga 240
tcgtcggctc aaccggttcc ataggaacac agacattgga catcgttgcg gagaatcctg 300
acaagttccg ggttgtcgct cttgctgctg ctccaatgt cactcttcta gctgatcagg 360
tgaaaacgtt caagccaaag ctggtggctg taagaaacga gtcattactt aacgagctaa 420
aggaagcgtt agctggttgt gaagaaatgc cggaaattat tcctggggag caaggtgtca 480
tagaggtcgc tcgccacccg gatgcagtta cagtcgttac gggcatagta gggtgtgcag 540

18

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gactcaagcc tacagttgca gcaattgaag ctgggaaaga tattgcgttg gcgaacaaag  600
agacacttat cgcaggcggt ccgttcgtgc ttccccttgc gcacaagcac aatgtgaaaa  660
tacttcctgc tgattcagag cactctgcaa tatttcagtg tatacaaggc ttgtctgaag  720
gatcacttcg tcgcgttatt ctgactgcgt ctggcggtgc tttcagggac tggccagttg  780
agaagctgaa agatgtaaag gttgccgatg ctttgaagca cccaaactgg agcatgggga  840
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<210> 20
<211> 473
<212> PRT
<213> Triticum aestivum

<400> 20
Thr Ser Ser Phe Ser Leu Leu Glu Leu Ser Ser Gly Thr Thr Arg Ser
  1               5                  10                  15

Arg Arg Gly Ala Ala Phe Arg Pro Arg Gln His Gln Arg Lys Val Asp
             20                  25                  30

Leu Thr Phe Gln Arg Arg Asp Lys Arg Ala Ala Tyr Leu Arg Thr Cys
         35                  40                  45

Cys Ser Met Gln Gln Gly Pro Pro Pro Ala Trp Pro Gly Arg Ala Val
     50                  55                  60

Ala Glu Pro Glu Arg Arg Ser Trp Glu Gly Pro Lys Pro Ile Ser Ile
 65                  70                  75                  80

Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala
             85                  90                  95

Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn
            100                 105                 110

Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu Val
            115                 120                 125

Ala Val Arg Asn Glu Ser Leu Leu Asn Glu Leu Lys Glu Ala Leu Ala
        130                 135                 140

Gly Cys Glu Glu Met Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile
145                 150                 155                 160

Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile Val
                165                 170                 175

Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys
```

```
                 180                    185                    190

Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe
        195                 200                 205

Val Leu Pro Leu Ala His Lys His Asn Val Lys Ile Leu Pro Ala Asp
        210                 215                 220

Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly
225                 230                 235                 240

Ser Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp
            245                 250                 255

Trp Pro Val Glu Lys Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys
            260                 265                 270

His Pro Asn Trp Ser Met Gly Lys Lys Ile Thr Val Asp Ser Ala Thr
            275                 280                 285

Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly
        290                 295                 300

Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile
305                 310                 315                 320

His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly
            325                 330                 335

Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp
            340                 345                 350

Arg Val Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys
            355                 360                 365

Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro Ser
        370                 375                 380

Val Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly
385                 390                 395                 400

Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu
            405                 410                 415

Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Met Thr Cys Asp
            420                 425                 430

Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile Ile
            435                 440                 445

His Tyr Asp Gln Trp Ala Arg Lys Phe Ala Ala Asn Leu Gln Pro Ser
        450                 455                 460

Ser Ser Gly Arg Ser Pro Val Leu Ala
465                 470

<210> 21
<211> 406
<212> PRT
<213> Arabidopsis thaliana
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20

<400> 21

Ala Pro Arg Gln Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
1   5   10   15

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
            20   25   30

Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
        35   40   45

Leu Leu Ala Asp Gln Val Arg Arg Phe Lys Pro Ala Leu Val Ala Val
    50   55   60

Arg Asn Glu Ser Leu Ile Asn Glu Leu Lys Glu Ala Leu Ala Asp Leu
65   70   75   80

Asp Tyr Lys Leu Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Val
            85   90   95

Ala Arg His Pro Glu Ala Val Thr Val Val Thr Gly Ile Val Gly Cys
        100   105   110

Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
    115   120   125

Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe Val Leu
    130   135   140

Pro Leu Ala Asn Lys His Asn Val Lys Ile Leu Pro Ala Asp Ser Glu
145   150   155   160

His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu Gly Ala Leu
            165   170   175

Arg Lys Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp Trp Pro
        180   185   190

Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu Lys His Pro
    195   200   205

Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala Thr Leu Phe
    210   215   220

Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Glu
225   230   235   240

Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
            245   250   255

Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly Trp Pro
        260   265   270

Asp Met Arg Leu Pro Ile Leu Tyr Thr Met Ser Trp Pro Asp Arg Val
        275   280   285

Pro Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys Leu Gly
    290   295   300

Ser Leu Thr Phe Lys Lys Pro Asp Asn Val Lys Tyr Pro Ser Met Asp

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Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu
            325                 330                 335

Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Ile Asp Glu Lys Ile
            340                 345                 350

Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asp Lys His
            355                 360                 365

Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Glu Ile Val His Tyr
            370                 375                 380

Asp Leu Trp Ala Arg Glu Tyr Ala Ala Asn Val Gln Leu Ser Ser Gly
385                 390                 395                 400

Ala Arg Pro Val His Ala
            405
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<210> 22
<211> 475
<212> PRT
<213> Mentha x piperita

<400> 22

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Met Ala Leu Asn Leu Met Ala Pro Thr Glu Ile Lys Thr Leu Ser Phe
  1               5                  10                  15

Leu Asp Ser Ser Lys Ser Asn Tyr Asn Leu Asn Pro Leu Lys Phe Gln
            20                  25                  30

Gly Gly Phe Ala Phe Lys Arg Lys Asp Ser Arg Cys Thr Ala Ala Lys
            35                  40                  45

Arg Val His Cys Ser Ala Gln Ser Gln Ser Pro Pro Pro Ala Trp Pro
      50                  55                  60

Gly Arg Ala Phe Pro Glu Pro Gly Arg Met Thr Trp Glu Gly Pro Lys
  65                  70                  75                  80

Pro Ile Ser Val Ile Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu
            85                  90                  95

Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Ile Val Ala Leu Ala
            100                 105                 110

Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Lys Ala Phe Lys Pro
            115                 120                 125

Lys Leu Val Ser Val Lys Asp Glu Ser Leu Ile Ser Glu Leu Lys Glu
            130                 135                 140

Ala Leu Ala Gly Phe Glu Asp Met Pro Glu Ile Ile Pro Gly Glu Gln
145                 150                 155                 160

Gly Met Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr
            165                 170                 175

Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu
```

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Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly
        195   200   205

Gly Pro Phe Val Leu Pro Leu Ala Lys Lys His Asn Val Lys Ile Leu
        210   215   220

Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu
225   230   235   240

Pro Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala
                245   250   255

Phe Arg Asp Leu Pro Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp
            260   265   270

Ala Leu Lys His Ser Asn Trp Asn Met Gly Lys Lys Asn Thr Val Arg
        275   280   285

Leu Leu Gln Leu Phe Phe Asn Lys Gly Leu Glu Val Ile Lys Ala His
        290   295   300

Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Ser
305   310   315   320

Pro Ser Ile Ile His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu
            325   330   335

Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu
        340   345   350

Ser Trp Pro Glu Arg Val Tyr Cys Ser Glu Ile Thr Trp Pro Arg Leu
        355   360   365

Asp Leu Cys Lys Val Asp Leu Pro Phe Lys Lys Pro Asp Asn Arg Glu
    370   375   380

Ile Pro Ala Met Asp Leu Ala Tyr Ala Ala Trp Lys Ser Arg Ser Thr
385   390   395   400

Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe
            405   410   415

Ile Asp Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu
        420   425   430

Thr Cys Asp Lys His Arg Ser Glu Met Ala Val Ser Pro Ser Leu Glu
        435   440   445

Glu Ile Val His Tyr Asp Gln Trp Ala Arg Asp Tyr Ala Ala Thr Val
    450   455   460

Leu Lys Ser Ala Gly Leu Ser Pro Ala Leu Val
465   470   475